EAST Search History

Ref #	Hits	Search Query	DBs	Default Operator	Plurals	Time Stamp
L1	11	CD80 same phage	US-PGPUB; USPAT; EPO; JPO; DERWENT	OR	OFF	2006/04/06 16:25
L2	0	CD80 same N2 same display	US-PGPUB; USPAT; EPO; JPO; DERWENT	OR	OFF	2006/04/06 16:25
L3	1	CD80 same N2	US-PGPUB; USPAT; EPO; JPO; DERWENT	OR	OFF	2006/04/06 16:26

EAST Search History

Ref #	Hits	Search Query	DBs	Default Operator	Plurals	Time Stamp
L1	1594	B7-1	US-PGPUB; USPAT; EPO; JPO; DERWENT	OR	OFF	2006/04/06 17:28
L2	12	(B7-1) same phage	US-PGPUB; USPAT; EPO; JPO; DERWENT	OR	OFF	2006/04/06 17:28

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 NEWS  1           Web Page URLs for STN Seminar Schedule - N. America
 NEWS  2           "Ask CAS" for self-help around the clock
 NEWS  3  DEC 21   IPC search and display fields enhanced in CA/CAplus with the
                   IPC reform
 NEWS  4  DEC 23   New IPC8 SEARCH, DISPLAY, and SELECT fields in USPATFULL/
                   USPAT2
 NEWS  5  JAN 13   IPC 8 searching in IFIPAT, IFIUDB, and IFICDB
 NEWS  6  JAN 13   New IPC 8 SEARCH, DISPLAY, and SELECT enhancements added to
                   INPADOC
 NEWS  7  JAN 17   Pre-1988 INPI data added to MARPAT
 NEWS  8  JAN 17   IPC 8 in the WPI family of databases including WPIFV
 NEWS  9  JAN 30   Saved answer limit increased
 NEWS 10  JAN 31   Monthly current-awareness alert (SDI) frequency
                   added to TULSA
 NEWS 11  FEB 21   STN AnaVist, Version 1.1, lets you share your STN AnaVist
                   visualization results
 NEWS 12  FEB 22   Status of current WO (PCT) information on STN
 NEWS 13  FEB 22   The IPC thesaurus added to additional patent databases on STN
 NEWS 14  FEB 22   Updates in EPFULL; IPC 8 enhancements added
 NEWS 15  FEB 27   New STN AnaVist pricing effective March 1, 2006
 NEWS 16  FEB 28   MEDLINE/LMEDLINE reload improves functionality
 NEWS 17  FEB 28   TOXCENTER reloaded with enhancements
 NEWS 18  FEB 28   REGISTRY/ZREGISTRY enhanced with more experimental spectral
                   property data
 NEWS 19  MAR 01   INSPEC reloaded and enhanced
 NEWS 20  MAR 03   Updates in PATDPA; addition of IPC 8 data without attributes
 NEWS 21  MAR 08   X.25 communication option no longer available after June 2006
 NEWS 22  MAR 22   EMBASE is now updated on a daily basis
 NEWS 23  APR 03   New IPC 8 fields and IPC thesaurus added to PATDPAFULL
 NEWS 24  APR 03   Bibliographic data updates resume; new IPC 8 fields and IPC
                   thesaurus added in PCTFULL
 NEWS 25  APR 04   STN AnaVist $500 visualization usage credit offered

 NEWS EXPRESS  FEBRUARY 15 CURRENT VERSION FOR WINDOWS IS V8.01a,
               CURRENT MACINTOSH VERSION IS V6.0c(ENG) AND V6.0Jc(JP),
               AND CURRENT DISCOVER FILE IS DATED 19 DECEMBER 2005.
               V8.0 AND V8.01 USERS CAN OBTAIN THE UPGRADE TO V8.01a AT
               http://download.cas.org/express/v8.0-Discover/

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FILE 'HOME' ENTERED AT 16:26:08 ON 06 APR 2006

=> file .meeting
'EVENTLINE' IS NOT A VALID FILE NAME
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that are available.  If you have requested multiple files, you can
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accessing the remaining file names entered.
ENTER A FILE NAME OR (IGNORE):ignore
'MEDICONF' IS NOT A VALID FILE NAME
Enter "HELP FILE NAMES" at an arrow prompt (=>) for a list of files
that are available.  If you have requested multiple files, you can
specify a corrected file name or you can enter "IGNORE" to continue
accessing the remaining file names entered.
ENTER A FILE NAME OR (IGNORE):ignore
COST IN U.S. DOLLARS                                SINCE FILE      TOTAL
                                                         ENTRY    SESSION
FULL ESTIMATED COST                                       0.21       0.21

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FILE 'BIOTECHNO' ENTERED AT 16:26:24 ON 06 APR 2006
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=> CD80 and phage
L1            0 FILE AGRICOLA
L2            6 FILE BIOTECHNO
L3            0 FILE CONFSCI
L4            0 FILE HEALSAFE
L5            0 FILE IMSDRUGCONF
L6            4 FILE LIFESCI
L7            0 FILE PASCAL

TOTAL FOR ALL FILES
L8           10 CD80 AND PHAGE

=> dup rem
ENTER L# LIST OR (END):l8
DUPLICATE IS NOT AVAILABLE IN 'IMSDRUGCONF'.
ANSWERS FROM THESE FILES WILL BE CONSIDERED UNIQUE
PROCESSING COMPLETED FOR L8
L9             6 DUP REM L8 (4 DUPLICATES REMOVED)

=> d l9 ibib abs total

L9   ' ANSWER 1 OF 6  BIOTECHNO  COPYRIGHT 2006 Elsevier Science B.V. on STN
       DUPLICATE
ACCESSION NUMBER:         2003:37314397   BIOTECHNO
TITLE:                    Inhibition of the CD28-CD80 co-stimulation
```

signal by a CD28-binding affibody ligand developed by combinatorial protein engineering
AUTHOR: Sandstrom K.; Xu Z.; Forsberg G.; Nygren P.-Å.
CORPORATE SOURCE: P.-Å. Nygren, Department of Biotechnology, Royal Institute of Technology, AlbaNova University Center, SE-106 90 Stockholm, Sweden.
E-mail: perake@biotech.kth.se
SOURCE: Protein Engineering, (2003), 16/9 (691-697), 37 reference(s)
CODEN: PRENE0 ISSN: 0269-2139
DOCUMENT TYPE: Journal; Article
COUNTRY: United Kingdom
LANGUAGE: English
SUMMARY LANGUAGE: English
AN 2003:37314397 BIOTECHNO
AB CD28 is one of the key molecules for co-stimulatory signalling in T cells. Here, novel ligands (affibodies) showing selective binding to human CD28 (hCD28) have been selected by **phage** display technology from a protein library constructed through combinatorial mutagenesis of a 58-residue three-helix bundle domain derived from staphylococcal protein A. Analysis of selected affibodies showed a marked sequence homology and biosensor analyses showed that all investigated affibodies bound to hCD28 with micromolar affinities (K .sub.D). No cross-reactivity towards the related protein human CTLA-4 could be observed. This lack of cross-reactivity to hCTLA-4 suggests that the recognition site on hCD28 for the affibodies resides outside the conserved MYPPPYY motif. The apparent binding affinity for hCD28 could be improved through fusion to an Fc fragment fusion partner, resulting in a divalent presentation of the affibody ligand. For the majority of selected anti-CD28 affibodies, in co-culture experiments involving Jurkat T-cells and CHO cell lines transfected to express human **CD80** (hCD80) or LFA-3 (hLFA-3) on the cell surface, respectively, pre-incubation of Jurkat cells with affibodies resulted in inhibition of IL-2 production when they were co-cultured with CHO (hCD80 .sup.+) cells, but not with CHO (hLFA-3.sup.+) cells. For one affibody variant denoted Z.sub.C.sub.D.sub.2.sub.8.sub.:.sub.5 a clear concentration-dependent inhibition was seen, indicating that this affibody binds hCD28 and specifically interferes in the interaction between hCD28 and hCD80.

L9 ANSWER 2 OF 6 BIOTECHNO COPYRIGHT 2006 Elsevier Science B.V. on STN DUPLICATE
ACCESSION NUMBER: 2001:32692572 BIOTECHNO
TITLE: Building novel binding ligands to B7.1 and B7.2 based on human antibody single variable light chain domains
AUTHOR: Van den Beucken T.; Van Neer N.; Sablon E.; Desmet J.; Celis L.; Hoogenboom H.R.; Hufton S.E.
CORPORATE SOURCE: H.R. Hoogenboom, Dyax B. V. Provisorium, PO Box 5800, 6202 AZ Maastricht, Netherlands.
E-mail: hhoogenboom@dyax.com
SOURCE: Journal of Molecular Biology, (13 JUL 2001), 310/3 (591-601), 41 reference(s)
CODEN: JMOBAK ISSN: 0022-2836
DOCUMENT TYPE: Journal; Article
COUNTRY: United Kingdom
LANGUAGE: English
SUMMARY LANGUAGE: English
AN 2001:32692572 BIOTECHNO
AB Ligands specific for B7.1 (**CD80**) and B7.2 (CD86) have applications in disease indications that require inhibition of T-cell activity. As we observed significant sequence and structural similarity between the B7-binding ligand, cytotoxic T-lymphocyte associated protein-4 (CTLA-4), and antibody variable light chain domains (VLs), we have explored the possibilities of making novel B7 binding molecules based on single VL domains. We first describe the "rational" design and construction of a VL/CTLA-4 hybrid molecule in which we have grafted both the CDR1 and CDR3-like loops of CTLA-4 onto a single VL light chain, at sites determined by sequence and structure-based alignment. This molecule was secreted as a soluble product from Escherichia coli, but did not show any binding to B7.1 and B7.2. In a second approach we constructed a VL

library in which human VL genes derived from B-cells were spiked with the CDR3-1ike loop of CTLA-4 and further diversified by DNA shuffling. This library was displayed on **phage**, and after selection gave B7.1 binding ligands which competed with CTLA-4. In order to evaluate the possible general utility of VL domains as binding ligands, we have constructed a non-biased VL library. From this DNA-shuffled human VL library we have selected single VL domains specific for B7.1, B7.2 or human IgG. Two B7.1-specific VL ligands and one B7.2-specific VL ligand showed competition with CTLA-4. One candidate VL domain-specific for B7.1 was affinity matured by simultaneous randomisation of all CDR loops using DNA shuffling with degenerate CDR-spiking oligonucleotides. From this library, a single VL domain with affinity of 191 nM for B7.1 was obtained, which also showed binding to B7.1 in situ. This VL had mutations in CDR1 and CDR3, indicating that antigen recognition for this single VL is most likely mediated by the same regions as in the VL domain of whole antibodies. The B7.1 and B7.2-specific VL domains described in this study may form the basis of a new family of immunomodulatory recombinant molecules. Furthermore, our studies suggest that it is feasible to create specific single VL domains to diverse targets as is the case for single VH domains.

L9 ANSWER 3 OF 6 BIOTECHNO
DUPLICATE
ACCESSION NUMBER: 2000:30150943 BIOTECHNO
TITLE: Molecular characterization and applications of recombinant scFv antibodies to CD152 co-stimulatory molecule
AUTHOR: Pistillo M.P.; Tazzari P.L.; Ellis J.H.; Ferrara G.B.
CORPORATE SOURCE: Dr. M.P. Pistillo, Lab. di Immunogenetica, Centro Biotecnologie Avanzate, Largo Rosanna Benzi 10, 16132 Genova, Italy.
E-mail: pistillo@ermes.cba.unige.it
SOURCE: Tissue Antigens, (2000), 55/3 (229-238), 27 reference(s)
CODEN: TSANA2 ISSN: 0001-2815
DOCUMENT TYPE: Journal; Article
COUNTRY: Denmark
LANGUAGE: English
SUMMARY LANGUAGE: English
AN 2000:30150943 BIOTECHNO
AB Recombinant human monoclonal antibodies against CD152 have been generated by selecting a synthetic **phage** scFv library with purified CD152-Ig fusion protein. Sixteen scFv fragments were isolated which specifically react with CD152 by enzyme-linked immunoabsorbent assay (ELISA) and Western blot resulting in their clustering into two groups recognizing different antigenic determinants. One group of scFvs (3, 13, 40, 44, 47, 51, 57, 80 83) recognized an epitope on CD152 dimer whereas another group (15, 18, 31, 35, 54, 72, 81) recognized an epitope on both dimeric and monomeric CD152 molecule suggesting their possible use in understanding the subunit structure of CD152 which is still controversial. Sequencing of the VH genes revealed that all the scFvs belonged to the VH3 gene family but they were different in CDR3 length and composition. It was possible to correlate specific CDR3 sequences with reactivity of the two groups of scFvs. Four scFvs, 3, 40, 81 and 83, each representative of one specific CDR3, were selected for further analysis. Competition ELISA experiments showed that they recognize CD152 in its native configuration and bound to different epitopes from the **CD80**/CD86 interaction site. The scFvs were able to stain human T lymphocytes stimulated either with anti-CD3 and CD28 antibodies or PHA, PMA and ionomycin by cytofluorimetry suggesting that they can be useful reagents for monitoring the kinetics of surface-bound and intracellular CD152.

L9 ANSWER 4 OF 6 BIOTECHNO
ACCESSION NUMBER: 2000:30408458 BIOTECHNO
TITLE: Development and application of cytotoxic T lymphocyte-associated antigen 4 as a protein scaffold for the generation of novel binding ligands
AUTHOR: Hufton S.E.; Van Neer N.; Van den Beuken T.; Desmet

J.; Sablon E.; Hoogenboom H.R.
CORPORATE SOURCE: H.R. Hoogenboom, Target Quest B.V., Provisorium, P.O. Box 5800, 6202 AZ Maastricht, Netherlands.
E-mail: hho@lpat.azm.nl
SOURCE: FEBS Letters, (23 JUN 2000), 475/3 (225-231), 30 reference(s)
CODEN: FEBLAL ISSN: 0014-5793
PUBLISHER ITEM IDENT.: S0014579300017014
DOCUMENT TYPE: Journal; Article
COUNTRY: Netherlands
LANGUAGE: English
SUMMARY LANGUAGE: English
AN 2000:30408458 BIOTECHNO
AB We have explored the possibilities of using human cytotoxic T lymphocyte-associated antigen 4 (CTLA-4) as a single immunoglobulin fold-based scaffold for the generation of novel binding ligands. To obtain a suitable protein library selection system, the extracellular domain of CTLA-4 was first displayed on the surface of a filamentous **phage** as a fusion product of the **phage** coat protein p3. CTLA-4 was shown to be functionally intact by binding to its natural ligands B7-1 (**CD80**) and B7-2 (CD86) both in vitro and in situ. Secondly, the complementarity determining region 3 (CDR3) loop of the CTLA-4 extracellular domain was evaluated as a permissive site. We replaced the nine amino acid CDR3-like loop of CTLA-4 with the sequence XXX- RGD-XXX (where X represents any amino acid). Using **phage** display we selected several CTLA-4-based variants capable of binding to human αvβ3 integrin, one of which showed binding to integrins in situ. To explore the construction of bispecific molecules we also evaluated one other potential permissive site diametrically opposite the natural CDR-like loops, which was found to be tolerant of peptide insertion. Our data suggest that CTLA-4 is a suitable human scaffold for engineering single-domain molecules with one or possibly more binding specificities. (C) 2000 Federation of European Biochemical Societies.

L9 ANSWER 5 OF 6 BIOTECHNO COPYRIGHT 2006 Elsevier Science B.V. on STN
ACCESSION NUMBER: 1999:29305090 BIOTECHNO
TITLE: Design and expression of soluble CTLA-4 variable domain as a scaffold for the display of functional polypeptides
AUTHOR: Nuttall S.D.; Rousch M.J.M.; Irving R.A.; Hufton S.E.; Hoogenboom H.R.; Hudson P.J.
CORPORATE SOURCE: S.D. Nuttall, CSIRO Molecular Science, 343 Royal Parade, Parkville, Vic. 3052, Australia.
E-mail: Stewart.Nuttall@molsci.csiro.au
SOURCE: Proteins: Structure, Function and Genetics, (01 AUG 1999), 36/2 (217-227), 50 reference(s)
CODEN: PSFGEY ISSN: 0887-3585
DOCUMENT TYPE: Journal; Article
COUNTRY: United States
LANGUAGE: English
SUMMARY LANGUAGE: English
AN 1999:29305090 BIOTECHNO
AB We have designed and engineered the human cytotoxic T-lymphocyte associated protein-4 (CTLA-4) variable (V-like) domain to produce a human- based protein scaffold for peptide display. First, to test whether the CTLA- 4 CDR-like loops were permissive to loop replacement/insertion we substituted either the CDR1 or CDR3 loop with somatostatin, a 14-residue intra-disulfide- linked neuropeptide. Upon expression as periplasmic-targeted proteins in Escherichia coli, molecules with superior solubility characteristics to the wild-type V-domain were produced. These mutations in CTLA-4 ablated binding to its natural ligands **CD80** and CD86, whereas binding to a conformation-dependent anti. CTLA-4 monoclonal antibody showed that the V-domain framework remained correctly folded. Secondly, to develop a system for library selection, we displayed both wild-type and mutated CTLA-4 proteins on the surface of fd-bacteriophage as fusions with the geneIII protein. CTLA-4 displayed on **phage** bound specifically to immobilized **CD80**-Ig and CD86-Ig and in one-step panning enriched 5,000 to 2,600-fold respectively over wild-type **phage**.

Bacteriophage displaying CTLA-4 with somatostatin in CDR3 (CTLA-4R- Som3) specifically bound somatostatin receptors on transfected CHO-K1 cells preincubated with 1μg/ml tunicamycin to remove receptor glycosylation. Binding was specific, as 1 μM somatostatin successfully competed with CTLA- 4R-Som3. CTLA-4R-Som3 also activated as well as binding preferentially to non-glycosylated receptor subtype Sst4. The ability to substitute CDP-like loops within CTLA-4 will enable design and construction of more complex libraries of single V-like domain binding molecules.

L9 ANSWER 6 OF 6 BIOTECHNO COPYRIGHT 2006 Elsevier Science B.V. on STN
DUPLICATE

ACCESSION NUMBER: 1998:28562203 BIOTECHNO
TITLE: T cell proliferation-augmenting activities of the gene 3 protein derived from a **phage** library clone with **CD80**-binding activity
AUTHOR: Fukumoto T.; Torigoe N.; Ito Y.; Kajiwara Y.; Sugimura K.
CORPORATE SOURCE: Dr. K. Sugimura, Department of Bioengineering, Faculty of Engineering, Kagoshima University, Korimoto, Kagoshima 890-0065, Japan.
E-mail: kazu@be.kagoshima-u.ac.jp
SOURCE: Journal of Immunology, (15 DEC 1998), 161/12 (6622-6628), 34 reference(s)
CODEN: JOIMA3 ISSN: 0022-1767
DOCUMENT TYPE: Journal; Article
COUNTRY: United States
LANGUAGE: English
SUMMARY LANGUAGE: English
AN 1998:28562203 BIOTECHNO
AB We have isolated a **phage** clone, F2, by panning a **phage** library with a CTLA4-conformation recognizing mAb (anti-CTLA4 mAb). The unique sequence of 15 amino acids with an internal disulfide bond was inserted in the gene 3 proteins of F2 **phage** clone (F2-g3p). We show here that 1) F2-g3p was recognized with anti-CTLA4 mAb but not with anti-CD28 mAb, and 2) F2-g3p bound to **CD80** but not to CD86. The surface plasmon resonance analysis showed that F2-g3p strongly bound **CD80**. F2-g3p inhibited the binding of CTLA4 to **CD80** but not to CD86. In contrast, F2-g3p weakly inhibited the binding of CD28 with **CD80**. When hen egg lysozyme (HEL)-primed lymph node cells were stimulated with HEL in the presence of F2-g3p in vitro, cell proliferation was highly potentiated. In the absence of antigenic stimulation, F2-g3p induced no T cell proliferation, indicating the costimulatory nature of F2- g3p. The T cell-augmenting activity of the F2 clone was eliminated when the F2 clone was preincubated with **CD80** -Ig before the addition to the cultures, indicating the involvement of **CD80**-binding in the F2-g3p-mediated immunopotentiation. Thus, the F2 motif conferred **CD80**-binding activity and an immunoregulatory function to the g3p.

=> CD80 and display and library
L10 0 FILE AGRICOLA
L11 4 FILE BIOTECHNO
L12 0 FILE CONFSCI
L13 0 FILE HEALSAFE
L14 0 FILE IMSDRUGCONF
L15 2 FILE LIFESCI
L16 0 FILE PASCAL

TOTAL FOR ALL FILES
L17 6 CD80 AND DISPLAY AND LIBRARY

=> dup rem
ENTER L# LIST OR (END):l17
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ANSWERS FROM THESE FILES WILL BE CONSIDERED UNIQUE
PROCESSING COMPLETED FOR L17
L18 5 DUP REM L17 (1 DUPLICATE REMOVED)

=> d l18 ibib abs total

L18 ANSWER 1 OF 5 BIOTECHNO COPYRIGHT 2006 Elsevier Science B.V. on STN
DUPLICATE
ACCESSION NUMBER: 2003:37314397 BIOTECHNO
TITLE: Inhibition of the CD28-**CD80** co-stimulation signal by a CD28-binding affibody ligand developed by combinatorial protein engineering
AUTHOR: Sandstrom K.; Xu Z.; Forsberg G.; Nygren P.-Å.
CORPORATE SOURCE: P.-Å. Nygren, Department of Biotechnology, Royal Institute of Technology, AlbaNova University Center, SE-106 90 Stockholm, Sweden.
E-mail: perake@biotech.kth.se
SOURCE: Protein Engineering, (2003), 16/9 (691-697), 37 reference(s)
CODEN: PRENE0 ISSN: 0269-2139
DOCUMENT TYPE: Journal; Article
COUNTRY: United Kingdom
LANGUAGE: English
SUMMARY LANGUAGE: English
AN 2003:37314397 BIOTECHNO
AB CD28 is one of the key molecules for co-stimulatory signalling in T cells. Here, novel ligands (affibodies) showing selective binding to human CD28 (hCD28) have been selected by phage **display** technology from a protein **library** constructed through combinatorial mutagenesis of a 58-residue three-helix bundle domain derived from staphylococcal protein A. Analysis of selected affibodies showed a marked sequence homology and biosensor analyses showed that all investigated affibodies bound to hCD28 with micromolar affinities (K .sub.D). No cross-reactivity towards the related protein human CTLA-4 could be observed. This lack of cross-reactivity to hCTLA-4 suggests that the recognition site on hCD28 for the affibodies resides outside the conserved MYPPPYY motif. The apparent binding affinity for hCD28 could be improved through fusion to an Fc fragment fusion partner, resulting in a divalent presentation of the affibody ligand. For the majority of selected anti-CD28 affibodies, in co-culture experiments involving Jurkat T-cells and CHO cell lines transfected to express human **CD80** (hCD80) or LFA-3 (hLFA-3) on the cell surface, respectively, pre-incubation of Jurkat cells with affibodies resulted in inhibition of IL-2 production when they were co-cultured with CHO (hCD80 .sup.+) cells, but not with CHO (hLFA-3.sup.+) cells. For one affibody variant denoted Z.sub.C.sub.D.sub.2.sub.8.sub.:.sub.5 a clear concentration-dependent inhibition was seen, indicating that this affibody binds hCD28 and specifically interferes in the interaction between hCD28 and hCD80.

L18 ANSWER 2 OF 5 BIOTECHNO COPYRIGHT 2006 Elsevier Science B.V. on STN
ACCESSION NUMBER: 2001:32692572 BIOTECHNO
TITLE: Building novel binding ligands to B7.1 and B7.2 based on human antibody single variable light chain domains
AUTHOR: Van den Beucken T.; Van Neer N.; Sablon E.; Desmet J.; Celis L.; Hoogenboom H.R.; Hufton S.E.
CORPORATE SOURCE: H.R. Hoogenboom, Dyax B. V. Provisorium, PO Box 5800, 6202 AZ Maastricht, Netherlands.
E-mail: hhoogenboom@dyax.com
SOURCE: Journal of Molecular Biology, (13 JUL 2001), 310/3 (591-601), 41 reference(s)
CODEN: JMOBAK ISSN: 0022-2836
DOCUMENT TYPE: Journal; Article
COUNTRY: United Kingdom
LANGUAGE: English
SUMMARY LANGUAGE: English
AN 2001:32692572 BIOTECHNO
AB Ligands specific for B7.1 (**CD80**) and B7.2 (CD86) have applications in disease indications that require inhibition of T-cell activity. As we observed significant sequence and structural similarity between the B7-binding ligand, cytotoxic T-lymphocyte associated protein-4 (CTLA-4), and antibody variable light chain domains (VLs), we have explored the possibilities of making novel B7 binding molecules

based on single VL domains. We first describe the "rational" design and construction of a VL/CTLA-4 hybrid molecule in which we have grafted both the CDR1 and CDR3-like loops of CTLA-4 onto a single VL light chain, at sites determined by sequence and structure-based alignment. This molecule was secreted as a soluble product from Escherichia coli, but did not show any binding to B7.1 and B7.2. In a second approach we constructed a VL **library** in which human VL genes derived from B-cells were spiked with the CDR3-like loop of CTLA-4 and further diversified by DNA shuffling. This **library** was displayed on phage, and after selection gave B7.1 binding ligands which competed with CTLA-4. In order to evaluate the possible general utility of VL domains as binding ligands, we have constructed a non-biased VL **library**. From this DNA-shuffled human VL **library** we have selected single VL domains specific for B7.1, B7.2 or human IgG. Two B7.1-specific VL ligands and one B7.2-specific VL ligand showed competition with CTLA-4. One candidate VL domain-specific for B7.1 was affinity matured by simultaneous randomisation of all CDR loops using DNA shuffling with degenerate CDR-spiking oligonucleotides. From this **library**, a single VL domain with affinity of 191 nM for B7.1 was obtained, which also showed binding to B7.1 in situ. This VL had mutations in CDR1 and CDR3, indicating that antigen recognition for this single VL is most likely mediated by the same regions as in the VL domain of whole antibodies. The B7.1 and B7.2-specific VL domains described in this study may form the basis of a new family of immunomodulatory recombinant molecules. Furthermore, our studies suggest that it is feasible to create specific single VL domains to diverse targets as is the case for single VH domains. .COPYRGT. 2001 Academic Press.

L18 ANSWER 3 OF 5 BIOTECHNO COPYRIGHT 2006 Elsevier Science B.V. on STN
ACCESSION NUMBER: 2000:30408458 BIOTECHNO
TITLE: Development and application of cytotoxic T lymphocyte-associated antigen 4 as a protein scaffold for the generation of novel binding ligands
AUTHOR: Hufton S.E.; Van Neer N.; Van den Beuken T.; Desmet J.; Sablon E.; Hoogenboom H.R.
CORPORATE SOURCE: H.R. Hoogenboom, Target Quest B.V., Provisorium, P.O. Box 5800, 6202 AZ Maastricht, Netherlands. E-mail: hho@lpat.azm.nl
SOURCE: FEBS Letters, (23 JUN 2000), 475/3 (225-231), 30 reference(s)
CODEN: FEBLAL ISSN: 0014-5793
PUBLISHER ITEM IDENT.: S0014579300017014
DOCUMENT TYPE: Journal; Article
COUNTRY: Netherlands
LANGUAGE: English
SUMMARY LANGUAGE: English
AN 2000:30408458 BIOTECHNO
AB We have explored the possibilities of using human cytotoxic T lymphocyte-associated antigen 4 (CTLA-4) as a single immunoglobulin fold-based scaffold for the generation of novel binding ligands. To obtain a suitable protein **library** selection system, the extracellular domain of CTLA-4 was first displayed on the surface of a filamentous phage as a fusion product of the phage coat protein p3. CTLA-4 was shown to be functionally intact by binding to its natural ligands B7-1 (**CD80**) and B7-2 (CD86) both in vitro and in situ. Secondly, the complementarity determining region 3 (CDR3) loop of the CTLA-4 extracellular domain was evaluated as a permissive site. We replaced the nine amino acid CDR3-like loop of CTLA-4 with the sequence XXX- RGD-XXX (where X represents any amino acid). Using phage **display** we selected several CTLA-4-based variants capable of binding to human αvβ3 integrin, one of which showed binding to integrins in situ. To explore the construction of bispecific molecules we also evaluated one other potential permissive site diametrically opposite the natural CDR-like loops, which was found to be tolerant of peptide insertion. Our data suggest that CTLA-4 is a suitable human scaffold for engineering single-domain molecules with one or possibly more binding specificities. (C) 2000 Federation of European Biochemical Societies.

L18 ANSWER 4 OF 5 BIOTECHNO COPYRIGHT 2006 Elsevier Science B.V. on STN

ACCESSION NUMBER: 1999:29305090 BIOTECHNO
TITLE: Design and expression of soluble CTLA-4 variable domain as a scaffold for the **display** of functional polypeptides
AUTHOR: Nuttall S.D.; Rousch M.J.M.; Irving R.A.; Hufton S.E.; Hoogenboom H.R.; Hudson P.J.
CORPORATE SOURCE: S.D. Nuttall, CSIRO Molecular Science, 343 Royal Parade, Parkville, Vic. 3052, Australia. E-mail: Stewart.Nuttall@molsci.csiro.au
SOURCE: Proteins: Structure, Function and Genetics, (01 AUG 1999), 36/2 (217-227), 50 reference(s) CODEN: PSFGEY ISSN: 0887-3585
DOCUMENT TYPE: Journal; Article
COUNTRY: United States
LANGUAGE: English
SUMMARY LANGUAGE: English
AN 1999:29305090 BIOTECHNO
AB We have designed and engineered the human cytotoxic T-lymphocyte associated protein-4 (CTLA-4) variable (V-like) domain to produce a human- based protein scaffold for peptide **display**. First, to test whether the CTLA- 4 CDR-like loops were permissive to loop replacement/insertion we substituted either the CDR1 or CDR3 loop with somatostatin, a 14-residue intra-disulfide- linked neuropeptide. Upon expression as periplasmic-targeted proteins in Escherichia coli, molecules with superior solubility characteristics to the wild-type V-domain were produced. These mutations in CTLA-4 ablated binding to its natural ligands **CD80** and CD86, whereas binding to a conformation- dependent anti. CTLA-4 monoclonal antibody showed that the V-domain framework remained correctly folded. Secondly, to develop a system for **library** selection, we displayed both wild-type and mutated CTLA-4 proteins on the surface of fd-bacteriophage as fusions with the geneIII protein. CTLA-4 displayed on phage bound specifically to immobilized **CD80**-Ig and CD86-Ig and in one-step panning enriched 5,000 to 2,600-fold respectively over wild-type phage. Bacteriophage displaying CTLA-4 with somatostatin in CDR3 (CTLA-4R- Som3) specifically bound somatostatin receptors on transfected CHO-K1 cells preincubated with 1μg/ml tunicamycin to remove receptor glycosylation. Binding was specific, as 1 μM somatostatin successfully competed with CTLA- 4R-Som3. CTLA-4R-Som3 also activated as well as binding preferentially to non-glycosylated receptor subtype Sst4. The ability to substitute CDP-like loops within CTLA-4 will enable design and construction of more complex **libraries** of single V-like domain binding molecules.

L18 ANSWER 5 OF 5 LIFESCI COPYRIGHT 2006 CSA on STN
ACCESSION NUMBER: 1999:27114 LIFESCI
TITLE: T Cell Proliferation-Augmenting Activities of the Gene 3 Protein Derived from a Phage **Library** Clone with **CD80**-Binding Activity
AUTHOR: Fukumoto, T.; Torigoe, N.; Ito, Y.; Kajiwara, Y.; Sugimura, K.*
CORPORATE SOURCE: Department of Bioengineering, Faculty of Engineering, Kagoshima University, Korimoto, Kagoshima, 890-0065, Japan; E-mail: kazu@be.kagoshima-u.ac.jp
SOURCE: Journal of Immunology, (19981215) vol. 161, no. 12, pp. 6622-6628. ISSN: 0022-1767.
DOCUMENT TYPE: Journal
FILE SEGMENT: F
LANGUAGE: English
SUMMARY LANGUAGE: English
AB We have isolated a phage clone, F2, by panning a phage **library** with a CTLA4-conformation recognizing mAb (anti-CTLA4 mAb). The unique sequence of 15 amino acids with an internal disulfide bond was inserted in the gene 3 proteins of F2 phage clone (F2-g3p). We show here that 1) F2-g3p was recognized with anti-CTLA4 mAb but not with anti-CD28 mAb, and 2) F2-g3p bound to **CD80** but not to CD86. The surface plasmon resonance analysis showed that F2-g3p strongly bound **CD80**. F2-g3p inhibited the binding of CTLA4 to **CD80** but not to CD86.

In contrast, F2-g3p weakly inhibited the binding of CD28 with **CD80**. When hen egg lysozyme (HEL)-primed lymph node cells were stimulated with HEL in the presence of F2-g3p in vitro, cell proliferation was highly potentiated. In the absence of antigenic stimulation, F2-g3p induced no T cell proliferation, indicating the costimulatory nature of F2-g3p. The T cell-augmenting activity of the F2 clone was eliminated when the F2 clone was preincubated with **CD80**-Ig before the addition to the cultures, indicating the involvement of **CD80**-binding in the F2-g3p-mediated immunopotentiation. Thus, the F2 motif conferred **CD80**-binding activity and an immunoregulatory function to the g3p.

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FILE 'HOME' ENTERED AT 16:05:04 ON 05 APR 2006

=> file .meeting
'EVENTLINE' IS NOT A VALID FILE NAME
Enter "HELP FILE NAMES" at an arrow prompt (=>) for a list of files
that are available.  If you have requested multiple files, you can
specify a corrected file name or you can enter "IGNORE" to continue
accessing the remaining file names entered.
ENTER A FILE NAME OR (IGNORE):ignore
'MEDICONF' IS NOT A VALID FILE NAME
Enter "HELP FILE NAMES" at an arrow prompt (=>) for a list of files
that are available.  If you have requested multiple files, you can
specify a corrected file name or you can enter "IGNORE" to continue
accessing the remaining file names entered.
ENTER A FILE NAME OR (IGNORE):ignore
COST IN U.S. DOLLARS                                SINCE FILE      TOTAL
                                                         ENTRY    SESSION
FULL ESTIMATED COST                                       0.21       0.21

FILE 'AGRICOLA' ENTERED AT 16:05:17 ON 05 APR 2006

FILE 'BIOTECHNO' ENTERED AT 16:05:17 ON 05 APR 2006
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=> N2-Vh-Vl
L1             0 FILE AGRICOLA
L2             0 FILE BIOTECHNO
L3             0 FILE CONFSCI
L4             0 FILE HEALSAFE
L5             0 FILE IMSDRUGCONF
L6             0 FILE LIFESCI
L7             0 FILE PASCAL

TOTAL FOR ALL FILES
L8             0 N2-VH-VL

=> N2-blocked
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L10            0 FILE BIOTECHNO
L11            0 FILE CONFSCI
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L13            0 FILE IMSDRUGCONF
L14            0 FILE LIFESCI
L15            0 FILE PASCAL

TOTAL FOR ALL FILES
L16            0 N2-BLOCKED

=> N2(3A)(block)
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L17           2 FILE AGRICOLA
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L19           0 FILE CONFSCI
L20           0 FILE HEALSAFE
L21           0 FILE IMSDRUGCONF
L22           2 FILE LIFESCI
L23           2 FILE PASCAL

TOTAL FOR ALL FILES
L24           6 N2(3A)(BLOCK)

=> dup rem
ENTER L# LIST OR (END):l24
DUPLICATE IS NOT AVAILABLE IN 'IMSDRUGCONF'.
ANSWERS FROM THESE FILES WILL BE CONSIDERED UNIQUE
PROCESSING COMPLETED FOR L24
L25            6 DUP REM L24 (0 DUPLICATES REMOVED)

=> d l25 ibib abs total

L25  ANSWER 1 OF 6  LIFESCI    COPYRIGHT 2006 CSA on STN
ACCESSION NUMBER:   2004:62421  LIFESCI
TITLE:              The Mad2 spindle checkpoint protein has two distinct
                    natively folded states
AUTHOR:             Luo, X.; Tang, Z.; Xia, G.; Wassmann, K.; Matsumoto, T.;
                    Rizo, J.; Yu, H.
CORPORATE SOURCE:   Department of Pharmacology, The University of Texas
                    Southwestern Medical Center, 5323 Harry Hines Boulevard,
                    Dallas, Texas 75390, USA.; E-mail: jose@arnie.swmed.edu or
                    Hongtao Yu
SOURCE:             Nature Structural & Molecular Biology [Nat. Struct. Mol.
                    Biol.], (20040400) vol. 11, no. 4, pp. 338-345.
                    ISSN: 1545-9993.
DOCUMENT TYPE:      Journal
FILE SEGMENT:       G
LANGUAGE:           English
SUMMARY LANGUAGE:   English
AB    The spindle checkpoint delays chromosome segregation in response to
      misaligned sister chromatids during mitosis, thus ensuring the fidelity of
      chromosome inheritance. Through binding to Cdc20, the Mad2 spindle
      checkpoint protein inhibits the target of this checkpoint, the ubiquitin
      protein ligase APC/C super(Cdc20). We now show that without cofactor
      binding or covalent modification Mad2 adopts two distinct folded
      conformations at equilibrium (termed N1-Mad2 and N2-Mad2). The structure
      of N2-Mad2 has been determined by NMR spectroscopy. N2-Mad2 is much more
      potent in APC/C inhibition. Overexpression of a Mad2 mutant that
      specifically sequesters N2-Mad2 partially blocks
      checkpoint signaling in living cells. The two Mad2 conformers interconvert
      slowly in vitro, but interconversion is accelerated by a fragment of Mad1,
      an upstream regulator of Mad2. Our results suggest that the unusual
      two-state behavior of Mad2 is critical for spindle checkpoint signaling.

L25  ANSWER 2 OF 6  LIFESCI    COPYRIGHT 2006 CSA on STN
ACCESSION NUMBER:   2003:72078  LIFESCI
TITLE:              Two Distinct Phases of Virus-induced Nuclear Factor  Kappa
                    B Regulation Enhance Tumor Necrosis Factor-related
                    Apoptosis-inducing Ligand-mediated Apoptosis in
                    Virus-infected Cells
AUTHOR:             Clarke, P.; Meintzer, S.M.; Moffitt, L.A.; Tyler, K.L.
CORPORATE SOURCE:   Departments of Neurology, Medicine, Microbiology, and
                    Immunology, University of Colorado Health Science Center,
                    Denver, Colorado; E-mail: Ken.Tyler@uchsc.edu
SOURCE:             Journal of Biological Chemistry [J. Biol. Chem.], (20030516
      )             vol. 278, no. 20, pp. 18092-18100.
                    ISSN: 0021-9258.
DOCUMENT TYPE:      Journal
FILE SEGMENT:       V; N
LANGUAGE:           English
SUMMARY LANGUAGE:   English
```

AB Cellular transcription factors are often utilized by infecting viruses to promote viral growth and influence cell fate. We have previously shown that nuclear factor Kappa B (NF- Kappa B) is activated after reovirus infection and that this activation is required for virus-induced apoptosis. In this report we identify a second phase of reovirus-induced NF- Kappa B regulation. We show that at later times post-infection NF-Kappa B activation is blocked in reovirus-infected cells. This results in the termination of virus-induced NF- Kappa B activity and the inhibition of tumor necrosis factor alpha and etoposide-induced NF- Kappa B activation in infected cells. Reovirus-induced inhibition of NF- Kappa B activation occurs by a mechanism that prevents I Kappa B alpha degradation and that is blocked in the presence of the viral RNA synthesis inhibitor, ribavirin. Reovirus-induced apoptosis is mediated by tumor necrosis factor-related apoptosis inducing ligand (TRAIL) in a variety of epithelial cell lines. Herein we show that ribavirin inhibits reovirus-induced apoptosis in TRAIL-resistant HEK293 cells and prevents the ability of reovirus infection to sensitize TRAIL-resistant cells to TRAIL-induced apoptosis. Furthermore, TRAIL-induced apoptosis is enhanced in HEK293 cells expressing I Kappa B[Delta]**N2**, which **blocks** NF- Kappa B activation. These results indicate that the ability of reovirus to inhibit NF- Kappa B activation sensitizes HEK293 cells to TRAIL and facilitates virus-induced apoptosis in TRAIL-resistant cells. Our findings demonstrate that two distinct phases of virus-induced NF- Kappa B regulation are required to efficiently activate host cell apoptotic responses to reovirus infection.

L25 ANSWER 3 OF 6 PASCAL COPYRIGHT 2006 INIST-CNRS. ALL RIGHTS RESERVED. on STN

ACCESSION NUMBER: 2000-0247593 PASCAL
TITLE (IN ENGLISH): Mass transfer of a penetrant plasticizer/simple gas mixture in a block copolymer
AUTHOR: SEMENOVA S. I.; SMIRNOV S. I.
CORPORATE SOURCE: Vladipore Research JSC, Vladimir, Russian Federation
SOURCE: Journal of Membrane Science, (2000), 168(1), 167-173, 8 refs.
ISSN: 0376-7388
DOCUMENT TYPE: Journal
BIBLIOGRAPHIC LEVEL: Analytic
COUNTRY: Netherlands
LANGUAGE: English
AVAILABILITY: INIST-17232

AN 2000-0247593 PASCAL
AB Mass transfer of a penetrant plasticizer/simple gas mixture in block copolymers with a flexible fragment and rigid fragment, the latter containing active groups that enter into donor-acceptor relation with the penetrant plasticizer, was investigated for the case of the systems comprising a mixture of SO2-N2/polyether (polyester) urethanes or polyether (polyester) urethane urea, polyarylate siloxanes having a block structure. Permeation of SO2 and **N2** in the **block** copolymers has been found to proceed through various fragments of polymer macromolecules.

L25 ANSWER 4 OF 6 AGRICOLA Compiled and distributed by the National Agricultural Library of the Department of Agriculture of the United States of America. It contains copyrighted materials. All rights reserved. (2006) on STN

ACCESSION NUMBER: 1998:36136 AGRICOLA
DOCUMENT NUMBER: IND20799746
TITLE: Development of a helium atmosphere soil incubation technique for direct measurement of nitrous oxide and dinitrogen fluxes during denitrification.
AUTHOR(S): Scholefield, D.; Hawkins, J.M.B.; Jackson, S.M.
SOURCE: Soil biology & biochemistry, Sept/Oct 1997. Vol. 29, No. 9/10. p. 1345-1352
Publisher: Oxford : Elsevier Science Ltd.
CODEN: SBIOAH; ISSN: 0038-0717
NOTE: Includes references
PUB. COUNTRY: England; United Kingdom
DOCUMENT TYPE: Article

FILE SEGMENT: Non-U.S. Imprint other than FAO
LANGUAGE: English
AB A technique is described in which the upper surfaces of intact soil cores are enveloped in a flowing atmosphere of He and O2 after first purging the soil and incubation vessel free from N2. This allows the independent measurement of N2O and N2 fluxes during denitrification of added or indigenous N03(-)-N by direct flushing to twin gas chromatographs and without recourse to acetylene blocking. Square section cores are extracted from random locations in the field and assembled without air gaps to make composite turves in the incubation vessel, thus preserving field aerobicity and orientation but allowing the spatial variability in denitrification to be accommodated. An N2-free irrigation assembly attached to each incubation vessel can be used to apply substrates during an experimental run, which is conducted in a temperature-controlled room. Use of the technique is demonstrated with measurements of N2O and N2 efflux from a wet, fine-textured soil under grassland management amended with nitrate and glucose. Peak concentrations were registered earlier than with previously-reported incubation techniques, with the flow rate of the incubation atmosphere having a substantial influence on the N2O to N2 ratio. Inclusion of acetylene as a component of the gas flow mixture stimulated denitrification and did not **block N2** production completely. Application of the technique is limited by the extent to which atmospheric N2 contamination can be reduced and ultimately by the sensitivity of the gas chromatograph. The system in its present form has a detection limit for N2 from denitrification of about 50 g N ha-1 d-1 and is therefore most suitably applied to soils under productive agricultural management.

L25 ANSWER 5 OF 6 PASCAL COPYRIGHT 2006 INIST-CNRS. ALL RIGHTS RESERVED. on STN
ACCESSION NUMBER: 1995-0589198 PASCAL
COPYRIGHT NOTICE: Copyright .COPYRGT. 1995 INIST-CNRS. All rights reserved.
TITLE (IN ENGLISH): Determination of myoglobin saturation of frozen specimens using a reflecting cryospectrophotometer
AUTHOR: VOTER W. A.; GAYESKI T. E. J.
CORPORATE SOURCE: Univ. Rochester medical cent., dep. anesthesiology, Rochester NY 14642, United States
SOURCE: American journal of physiology. Heart and circulatory physiology, (1995), 38(4), H1328-H1341, 33 refs. ISSN: 0363-6135 CODEN: AJPPDI
DOCUMENT TYPE: Journal
BIBLIOGRAPHIC LEVEL: Analytic
COUNTRY: United States
LANGUAGE: English
AVAILABILITY: INIST-670D, 354000050338330190
AN 1995-0589198 PASCAL
CP Copyright .COPYRGT. 1995 INIST-CNRS. All rights reserved.
AB This report describes a method and instrumentation for determining myoglobin (Mb) oxygen saturation in skeletal muscle. Canine gracilis is frozen in situ using a liquid **N2**-cooled copper **block**. Transverse section surfaces of frozen unstained muscle are observed at -110°C using a microspectrophotometric system. The Mb saturation is determined using epi-illumination and a four-wavelength optical method. A special aperture permits illumination of a 20-μm-square area, and the radius of the catchment volume is estimated to be .eqvsim. 60 μm, with the strongest signal arising from the central region. The equibestic wavelengths used were 546.6, 570.5, and 584.1 nm. The method was validated using the nonlinear multicomponent analysis method of Luebbers. End-point (0 and 100% saturation) calibration was set using ischemic and adenosine-treated highly oxygenated muscles, respectively. The effects of hemoglobin (Hb) and metmyoglobin (metMb) signal contamination were evaluated experimentally and by computer-mixing simulations. Mb saturation determinations adjacent to large vessels are to be avoided. MetMb and capillary Hb do not interfere with the determination. The reproducibility of the method is estimated to be ± 5%.

L25 ANSWER 6 OF 6 AGRICOLA Compiled and distributed by the National

ACCESSION NUMBER: 95:11952 AGRICOLA
DOCUMENT NUMBER: IND20443867
TITLE: Partial characterization of volatile fungistatic compound(s) from soil.
AUTHOR(S): Liebman, J.A.; Epstein, L.
CORPORATE SOURCE: University of California, Berkeley
AVAILABILITY: DNAL (464.8 P56)
SOURCE: Phytopathology, May 1994. Vol. 84, No. 5. p. 442-446
Publisher: St. Paul, Minn. : American Phytopathological Society, 1911-
CODEN: PHYTAJ; ISSN: 0031-949X
NOTE: Includes references
PUB. COUNTRY: Minnesota; United States
DOCUMENT TYPE: Article
FILE SEGMENT: U.S. Imprints not USDA, Experiment or Extension
LANGUAGE: English

AB Many soils contain volatile, water-soluble compound(s) that inhibit germination of Cochliobolus victoriae conidia in the absence of a carbon source. The volatile fungistatic compound(s) from soil were separated into a cell-free extract. Loss of fungistatic activity from the extract was time- and temperature-dependent; all activity was lost within 5 min at 90 C, 48 h at 21 C, and 5 days at -70 C. Much of the fungistatic activity was lost after the soil extract was diluted by 10%, incubated in an uncapped vial, or transferred to a new vial via a gas-tight syringe. Fungistatic activity was not detected in material collected from soil into a liquid **N2** cold trap. Agarose **blocks** adjusted to pH 5.5-8.0 became fungistatic when incubated on soil, suggesting that the fungistatic compound(s) were relatively unaffected by hydrogen ion concentrations in this range. Carbon monoxide (CO), carbon dioxide (CO2), nitric oxide (NO), nitrogen dioxide (NO2), sulfur dioxide (SO2), ammonia (NH3), ethylene (C2H4), and reduced concentrations of oxygen (O2) apparently were not responsible for fungistasis of C. victoriae conidia in soil because these compounds were not fungistatic at concentrations detected in soil.

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=> scFv and fragment and region and
MISSING TERM AFTER REGION AND
Operators must be followed by a search term, L-number, or query name.

=> scFv and fragment and region
L26           7 FILE AGRICOLA
L27         298 FILE BIOTECHNO
L28           0 FILE CONFSCI
L29           0 FILE HEALSAFE
L30           0 FILE IMSDRUGCONF
L31         179 FILE LIFESCI
L32         145 FILE PASCAL

TOTAL FOR ALL FILES
L33         629 SCFV AND FRAGMENT AND REGION

=> l33 and N2
L34           0 FILE AGRICOLA
L35           0 FILE BIOTECHNO
L36           0 FILE CONFSCI
L37           0 FILE HEALSAFE
L38           0 FILE IMSDRUGCONF
L39           0 FILE LIFESCI
L40           0 FILE PASCAL

TOTAL FOR ALL FILES
L41           0 L33 AND N2

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L43          14 FILE BIOTECHNO
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L44           2 FILE CONFSCI
L45           0 FILE HEALSAFE
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L46           0 FILE IMSDRUGCONF
L47          16 FILE LIFESCI
L48           8 FILE PASCAL

TOTAL FOR ALL FILES
L49          40 KUFER P/AU

=> raum t/au
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L51           3 FILE BIOTECHNO
L52           4 FILE CONFSCI
L53           0 FILE HEALSAFE
'AU' IS NOT A VALID FIELD CODE
L54           0 FILE IMSDRUGCONF
L55           2 FILE LIFESCI
L56           2 FILE PASCAL

TOTAL FOR ALL FILES
L57          11 RAUM T/AU

=> l49 and l57
L58           0 FILE AGRICOLA
L59           3 FILE BIOTECHNO
L60           0 FILE CONFSCI
L61           0 FILE HEALSAFE
L62           0 FILE IMSDRUGCONF
L63           2 FILE LIFESCI
L64           0 FILE PASCAL

TOTAL FOR ALL FILES
L65           5 L49 AND L57

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ENTER L# LIST OR (END):l65
DUPLICATE IS NOT AVAILABLE IN 'IMSDRUGCONF'.
ANSWERS FROM THESE FILES WILL BE CONSIDERED UNIQUE
PROCESSING COMPLETED FOR L65
L66           3 DUP REM L65 (2 DUPLICATES REMOVED)

=> d l66 ibib abs total

L66   ANSWER 1 OF 3  BIOTECHNO  COPYRIGHT 2006 Elsevier Science B.V. on STN
ACCESSION NUMBER:         2002:34602073   BIOTECHNO
TITLE:                    In vitro and in vivo activity of MT201, a fully human
                          monoclonal antibody for pancarcinoma treatment
AUTHOR:                   Naundorf S.; Preithner S.; Mayer P.; Lippold S.; Wolf
                          A.; Hanakan F.; Fichtner I.; Kufer P.;
                          Raum T.; Riethmuller G.; Baeuerle P.A.; Dreier
                          T.
CORPORATE SOURCE:         P.A. Baeuerle, Micromet AG, Am Klopferspitz 19, 82152
                          Martinsried, Germany.
                          E-mail: patrick.baeuerle@micromet.de
SOURCE:                   International Journal of Cancer, (01 JUL 2002), 100/1
                          (101-110), 44 reference(s)
                          CODEN: IJCNAW  ISSN: 0020-7136
DOCUMENT TYPE:            Journal; Article
COUNTRY:                  United States
LANGUAGE:                 English
SUMMARY LANGUAGE:         English
AN    2002:34602073   BIOTECHNO
AB    In our study, a novel, fully human, recombinant monoclonal antibody of
      the IgG1 isotype, called MT201, was characterized for its binding
      properties, complement-dependent (CDC) and antibody-dependent cellular
      cytotoxicity (ADCC), as well as for its in vivo antitumor activity in a
      nude mouse model. MT201 was found to bind its target, the epithelial cell
      adhesion molecule (Ep-CAM; also called 17-1A antigen, KSA, EGP-2,
```

GA733-2), with low affinity in a range similar to that of the clinically validated, murine monoclonal IgG2a antibody edrecolomab (Panorex®). MT201 exhibited Ep-CAM-specific CDC with a potency similar to that of edrecolomab. However, the efficacy of ADCC of MT201, as mediated by human immune effector cells, was by 2 orders of magnitude higher than that of edrecolomab. Addition of human serum reduced the ADCC of MT201 while it essentially abolished ADCC of edrecolomab within the concentration range tested. In a nude mouse xenograft model, growth of tumors derived from the human colon carcinoma line HT-29 was significantly and comparably suppressed by MT201 and edrecolomab. The fully human nature and the improved ADCC of MT201 with human effector cells will make MT201 a promising candidate for the clinical development of a novel pan-carcinoma antibody that is superior to edrecolomab. .COPYRGT. 2002 Wiley-Liss, Inc.

L66 ANSWER 2 OF 3 BIOTECHNO COPYRIGHT 2006 Elsevier Science B.V. on STN
DUPLICATE

ACCESSION NUMBER: 2001:32592061 BIOTECHNO
TITLE: Bispecific single-chain antibodies as effective tools for eliminating epithelial cancer cells from human stem cell preparations by redirected cell cytotoxicity
AUTHOR: Maletz K.; **Kufer P.**; Mack M.; **Raum T.**; Pantel K.; Riethmuller G.; Gruber R.
CORPORATE SOURCE: R. Gruber, Institut fur Immunologie, Mediz. Polik. Lud.-Maxi.-Univ. Munc., Ziemssenstr. 1, 80336 Munchen, Germany.
E-mail: Rudolf.Gruber@pk-i.med.uni-muenchen.de
SOURCE: International Journal of Cancer, (01 AUG 2001), 93/3 (409-416), 37 reference(s)
CODEN: IJCNAW ISSN: 0020-7136
DOCUMENT TYPE: Journal; Article
COUNTRY: United States
LANGUAGE: English
SUMMARY LANGUAGE: English
AN 2001:32592061 BIOTECHNO
AB High-dose chemotherapy (HDC) with autologous bone marrow or peripheral stem cell transplantation is discussed as one option to treat the extensive stage of a variety of tumors. Effective methods to eliminate contaminating tumor cells from human bone marrow or stem cell grafts may improve the outcome of the patients. We investigated 3 recombinant bispecific single-chain antibodies (bscAbs) directed against 17-1A (EpCAM), c-erbB-2 (HER-2/neu) and LeY on the one and CD3 on the other binding site for their ability to induce lysis of epithelial tumor cells by retargeting autochthonous T lymphocytes present in bone marrow mononuclear cells (BMMC) and in peripheral stem cell mononuclear cells (PSMC). The bscAbs showed remarkable specific lysis of different epithelial tumor cell lines with BMMCs as well as with PSMCs as effector cells. Investigation of the α17-1A-αCD3 bscAb revealed a significant correlation between the percentage of CD3.sup.+ cells present in the BMMCs and the rate of lysis as well as the absence of detrimental effects on the viability of hematopoietic progenitor cells as determined by colony-forming unit assays (CFUs). Our results indicate that recombinant bispecific single-chain antibodies could be new tools for purging of human bone marrow and peripheral stem cell grafts from contaminating epithelial cancer cells for patients receiving autologous stem cell transplantation after HDC. .COPYRGT. 2001 Wiley-Liss, Inc.

L66 ANSWER 3 OF 3 BIOTECHNO COPYRIGHT 2006 Elsevier Science B.V. on STN
DUPLICATE

ACCESSION NUMBER: 2001:32480558 BIOTECHNO
TITLE: Anti-self antibodies selected from a human IgD heavy chain repertoire: A novel approach to generate therapeutic human antibodies against tumor-associated differentiation antigens
AUTHOR: **Raum T.**; Gruber R.; Riethmuller G.; **Kufer P.**
CORPORATE SOURCE: P. Kufer, Institut fur Immunologie, Goethestrasse 31, 80336 Munich, Germany.
E-mail: Kufer@ifi.med.uni-muenchen.de
SOURCE: Cancer Immunology, Immunotherapy, (2001), 50/3

(141-150), 43 reference(s)
CODEN: CIIMDN ISSN: 0340-7004
DOCUMENT TYPE: Journal; Article
COUNTRY: Germany, Federal Republic of
LANGUAGE: English
SUMMARY LANGUAGE: English
AN 2001:32480558 BIOTECHNO
AB Human antibodies were isolated by phage display from a naturally expressed human antibody repertoire. Antibody selection was carried out against the epithelial cell adhesion molecule (EpCAM) or 17-1A antigen, that in a clinical trial had been successfully used as a target for antibody therapy of minimal residual colorectal cancer. VH chains were selected from the human IgD repertoire expressed on naive B2 and autoreactive B1 lymphocytes. By guiding the selection through a murine template antibody, two EpCAM-specific human antibodies, HD69 and HD70, were obtained that closely resembled the murine therapeutic 17-1A antibody in their binding properties when expressed as complete huIgG1 molecules in CHO cells. However, both human antibodies recruited human cytotoxic effector cells far more efficiently than the murine 17-1A antibody used for clinical trials. Therefore, and in view of the long in vivo half-life of human IgG1 antibodies, HD69 and HD70 are regarded as highly promising third generation versions of the murine therapeutic antibody. Because of their origin from an evolutionary conserved germline VH repertoire, they are expected to exhibit minimal immunogenicity in patients.

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 NEWS  1           Web Page URLs for STN Seminar Schedule - N. America
 NEWS  2           "Ask CAS" for self-help around the clock
 NEWS  3  DEC 21   IPC search and display fields enhanced in CA/CAplus with the
                   IPC reform
 NEWS  4  DEC 23   New IPC8 SEARCH, DISPLAY, and SELECT fields in USPATFULL/
                   USPAT2
 NEWS  5  JAN 13   IPC 8 searching in IFIPAT, IFIUDB, and IFICDB
 NEWS  6  JAN 13   New IPC 8 SEARCH, DISPLAY, and SELECT enhancements added to
                   INPADOC
 NEWS  7  JAN 17   Pre-1988 INPI data added to MARPAT
 NEWS  8  JAN 17   IPC 8 in the WPI family of databases including WPIFV
 NEWS  9  JAN 30   Saved answer limit increased
 NEWS 10  JAN 31   Monthly current-awareness alert (SDI) frequency
                   added to TULSA
 NEWS 11  FEB 21   STN AnaVist, Version 1.1, lets you share your STN AnaVist
                   visualization results
 NEWS 12  FEB 22   Status of current WO (PCT) information on STN
 NEWS 13  FEB 22   The IPC thesaurus added to additional patent databases on STN
 NEWS 14  FEB 22   Updates in EPFULL; IPC 8 enhancements added
 NEWS 15  FEB 27   New STN AnaVist pricing effective March 1, 2006
 NEWS 16  FEB 28   MEDLINE/LMEDLINE reload improves functionality
 NEWS 17  FEB 28   TOXCENTER reloaded with enhancements
 NEWS 18  FEB 28   REGISTRY/ZREGISTRY enhanced with more experimental spectral
                   property data
 NEWS 19  MAR 01   INSPEC reloaded and enhanced
 NEWS 20  MAR 03   Updates in PATDPA; addition of IPC 8 data without attributes
 NEWS 21  MAR 08   X.25 communication option no longer available after June 2006
 NEWS 22  MAR 22   EMBASE is now updated on a daily basis
 NEWS 23  APR 03   New IPC 8 fields and IPC thesaurus added to PATDPAFULL
 NEWS 24  APR 03   Bibliographic data updates resume; new IPC 8 fields and IPC
                   thesaurus added in PCTFULL
 NEWS 25  APR 04   STN AnaVist $500 visualization usage credit offered

 NEWS EXPRESS  FEBRUARY 15 CURRENT VERSION FOR WINDOWS IS V8.01a,
               CURRENT MACINTOSH VERSION IS V6.0c(ENG) AND V6.0Jc(JP),
               AND CURRENT DISCOVER FILE IS DATED 19 DECEMBER 2005.
               V8.0 AND V8.01 USERS CAN OBTAIN THE UPGRADE TO V8.01a AT
               http://download.cas.org/express/v8.0-Discover/

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FILE 'HOME' ENTERED AT 17:30:43 ON 06 APR 2006

=> file .meeting
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FULL ESTIMATED COST                                       0.21       0.21

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=> B7-1 and phage
L1             0 FILE AGRICOLA
L2             3 FILE BIOTECHNO
L3             0 FILE CONFSCI
L4             0 FILE HEALSAFE
L5             0 FILE IMSDRUGCONF
L6             1 FILE LIFESCI
L7             1 FILE PASCAL

TOTAL FOR ALL FILES
L8             5 B7-1 AND PHAGE

=> dup rem
ENTER L# LIST OR (END):l8
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L9              4 DUP REM L8 (1 DUPLICATE REMOVED)

=> d l9 ibib abs total

L9    ANSWER 1 OF 4  PASCAL  COPYRIGHT 2006 INIST-CNRS. ALL RIGHTS RESERVED. on
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ACCESSION NUMBER:         2005-0384182   PASCAL
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reserved.
TITLE (IN ENGLISH): Impaired capacity for upregulation of MHC class II in tumor-associated microglia
AUTHOR: SCHARTNER Jill M.; HAGAR Aaron R.; VAN HANDEL Michelle; LEYING ZHANG; NADKARNI Nivedita; BADIE Behnam
CORPORATE SOURCE: Department of Neurological Surgery, University of Wisconsin School of Medicine, Madison, Wisconsin, United States; Department of Biostatistics and Medical Informatics, University of Wisconsin School of Medicine, Madison, Wisconsin, United States
SOURCE: Glia : (New York, NY. Print), (2005), 51(4), 279-285, 31 refs.
ISSN: 0894-1491
DOCUMENT TYPE: Journal
BIBLIOGRAPHIC LEVEL: Analytic
COUNTRY: United States
LANGUAGE: English
AVAILABILITY: INIST-21570, 354000138448410040
AN 2005-0384182 PASCAL
CP Copyright .COPYRGT. 2005 INIST-CNRS. All rights reserved.
AB Immunotherapy for malignant gliomas is being studied as a possible adjunctive therapy for this highly fatal disease. Thus far, inadequate understanding of brain tumor immunology has hindered the design of such therapies. For instance, the role of microglia and macrophages, which comprise a significant proportion of tumor-infiltrating inflammatory cells, in the regulation of the local anti-tumor immune response is poorly understood. To study the response of microglia and macrophages to known activators in brain tumors, we injected CpG oligodeoxynucleotide (ODN), interferon-γ (IFN-γ), and IFN-γ/LPS into normal and intracranial RG2 glioma-bearing rodents. Microglia/ macrophage infiltration and their surface expression of MHC class II **B7**.
1 and B7.2 was examined by flow cytometry. Each agent evaluated yielded a distinct microglia/ macrophage response: CpG ODN was the most potent inducer of microglia/macrophage infiltration and **B7**.
1 expression, while IFN-γ resulted in the highest MHC-II expression in both normal and tumors. Regardless of the agent injected, however, MHC-II induction was significantly muted in tumor microglia/macrophage as compared with normal brain. These data suggest that microglia/macro-**phage** responsiveness to activators can vary in brain tumors when compared with normal brain. Understanding the mechanism of these differences may be critical in the development of novel immunotherapies for malignant glioma.

L9 ANSWER 2 OF 4 BIOTECHNO COPYRIGHT 2006 Elsevier Science B.V. on STN
ACCESSION NUMBER: 2001:32114675 BIOTECHNO
TITLE: The potent adjuvant activity of archaeosomes correlates to the recruitment and activation of macrophages and dendritic cells in vivo
AUTHOR: Krishnan L.; Sad S.; Patel G.B.; Sprott G.D.
CORPORATE SOURCE: Dr. L. Krishnan, National Research Council, Institute for Biological Sciences, 100 Sussex Drive, Ottawa, Ont. K1A 0R6, Canada.
E-mail: lakshmi.krishnan@nrc.ca
SOURCE: Journal of Immunology, (01 FEB 2001), 166/3 (1885-1893), 47 reference(s)
CODEN: JOIMA3 ISSN: 0022-1767
DOCUMENT TYPE: Journal; Article
COUNTRY: United States
LANGUAGE: English
SUMMARY LANGUAGE: English
AN 2001:32114675 BIOTECHNO
AB The unique glycerolipids of Archaea can be formulated into vesicles (archaeosomes) with potent adjuvant activity. We studied the effect of archaeosomes on APCs to elucidate the mechanism(s) of adjuvant action. Exposure of J774A.1 macrophages to archaeosomes in vitro resulted in up-regulation of **B7.1**, B7.2, and MHC class II molecules to an extent comparable to that achieved with LPS. Similarly, incubation of bone marrow-derived DCs with archaeosomes resulted in

enhanced expression of MHC class II and B7.2 molecules. In contrast, conventional liposomes made from ester phospholipids failed to modulate the expression of these activation markers. APCs treated with archaeosomes exhibited increased TNF production and functional ability to stimulate allogenic T cell proliferation. More interestingly, archaeosomes enhanced APC recruitment and activation in vivo. Intraperitoneal injection of archaeosomes into mice led to recruitment of Mac1α.sup.+, F4/80.sup.+ and CD11c.sup.+ cells. The expression of MHC class II on the surface of peritoneal cells was also enhanced. Furthermore, peritoneal cells from archaeosome-injected mice strongly enhanced allo-T cell proliferation and cytokine production. The ability of archaeosome-treated APCs to stimulate T cells was restricted to Mac1α.sup.h.sup.i.sup.g.sup.h, B220.sup.- cells in the peritoneum. These Mac1α.sup.h.sup.i.sup.g.sup.h cells in the presence of GM-CSF gave rise to both F4/80.sup.+ (macro-**phage**) and CD11c.sup.+ (dendritic) populations. Overall, the activation of APCs correlated to the ability of archaeosomes to induce strong humoral, T helper, and CTL responses to entrapped Ag. Thus, the recruitment and activation of professional APCs by archaeosomes constitutes an efficient self-adjuvanting process for induction of Ag-specific responses to encapsulated Ags.

L9 ANSWER 3 OF 4 BIOTECHNO COPYRIGHT 2006 Elsevier Science B.V. on STN
DUPLICATE
ACCESSION NUMBER: 2001:32692572 BIOTECHNO
TITLE: Building novel binding ligands to **B7**.**1** and B7.2 based on human antibody single variable light chain domains
AUTHOR: Van den Beucken T.; Van Neer N.; Sablon E.; Desmet J.; Celis L.; Hoogenboom H.R.; Hufton S.E.
CORPORATE SOURCE: H.R. Hoogenboom, Dyax B. V. Provisorium, PO Box 5800, 6202 AZ Maastricht, Netherlands.
E-mail: hhoogenboom@dyax.com
SOURCE: Journal of Molecular Biology, (13 JUL 2001), 310/3 (591-601), 41 reference(s)
CODEN: JMOBAK ISSN: 0022-2836
DOCUMENT TYPE: Journal; Article
COUNTRY: United Kingdom
LANGUAGE: English
SUMMARY LANGUAGE: English
AN 2001:32692572 BIOTECHNO
AB Ligands specific for **B7**.**1** (CD80) and B7.2 (CD86) have applications in disease indications that require inhibition of T-cell activity. As we observed significant sequence and structural similarity between the B7-binding ligand, cytotoxic T-lymphocyte associated protein-4 (CTLA-4), and antibody variable light chain domains (VLs), we have explored the possibilities of making novel B7 binding molecules based on single VL domains. We first describe the "rational" design and construction of a VL/CTLA-4 hybrid molecule in which we have grafted both the CDR1 and CDR3-like loops of CTLA-4 onto a single VL light chain, at sites determined by sequence and structure-based alignment. This molecule was secreted as a soluble product from Escherichia coli, but did not show any binding to **B7**.**1** and B7.2. In a second approach we constructed a VL library in which human VL genes derived from B-cells were spiked with the CDR3-like loop of CTLA-4 and further diversified by DNA shuffling. This library was displayed on **phage**, and after selection gave **B7**.**1** binding ligands which competed with CTLA-4. In order to evaluate the possible general utility of VL domains as binding ligands, we have constructed a non-biased VL library. From this DNA-shuffled human VL library we have selected single VL domains specific for **B7**.**1**, B7.2 or human IgG. Two **B7**.**1**-specific VL ligands and one B7.2-specific VL ligand showed competition with CTLA-4. One candidate VL domain-specific for **B7**.**1** was affinity matured by simultaneous randomisation of all CDR loops using DNA shuffling with degenerate CDR-spiking oligonucleotides. From this library, a single VL domain with affinity of 191 nM for **B7**.**1** was obtained, which also showed binding to **B7**.**1** in situ. This VL had mutations in CDR1 and CDR3, indicating that antigen recognition for this single VL

is most likely mediated by the same regions as in the VL domain of whole antibodies. The **B7.1** and B7.2-specific VL domains described in this study may form the basis of a new family of immunomodulatory recombinant molecules. Furthermore, our studies suggest that it is feasible to create specific single VL domains to diverse targets as is the case for single VH domains. .COPYRGT. 2001 Academic Press.

L9 ANSWER 4 OF 4 BIOTECHNO COPYRIGHT 2006 Elsevier Science B.V. on STN
ACCESSION NUMBER: 2000:30408458 BIOTECHNO
TITLE: Development and application of cytotoxic T lymphocyte-associated antigen 4 as a protein scaffold for the generation of novel binding ligands
AUTHOR: Hufton S.E.; Van Neer N.; Van den Beuken T.; Desmet J.; Sablon E.; Hoogenboom H.R.
CORPORATE SOURCE: H.R. Hoogenboom, Target Quest B.V., Provisorium, P.O. Box 5800, 6202 AZ Maastricht, Netherlands. E-mail: hho@lpat.azm.nl
SOURCE: FEBS Letters, (23 JUN 2000), 475/3 (225-231), 30 reference(s)
CODEN: FEBLAL ISSN: 0014-5793
PUBLISHER ITEM IDENT.: S0014579300017014
DOCUMENT TYPE: Journal; Article
COUNTRY: Netherlands
LANGUAGE: English
SUMMARY LANGUAGE: English
AN 2000:30408458 BIOTECHNO
AB We have explored the possibilities of using human cytotoxic T lymphocyte-associated antigen 4 (CTLA-4) as a single immunoglobulin fold-based scaffold for the generation of novel binding ligands. To obtain a suitable protein library selection system, the extracellular domain of CTLA-4 was first displayed on the surface of a filamentous **phage** as a fusion product of the **phage** coat protein p3. CTLA-4 was shown to be functionally intact by binding to its natural ligands **B7-1** (CD80) and B7-2 (CD86) both in vitro and in situ. Secondly, the complementarity determining region 3 (CDR3) loop of the CTLA-4 extracellular domain was evaluated as a permissive site. We replaced the nine amino acid CDR3-like loop of CTLA-4 with the sequence XXX- RGD-XXX (where X represents any amino acid). Using **phage** display we selected several CTLA-4-based variants capable of binding to human αvβ3 integrin, one of which showed binding to integrins in situ. To explore the construction of bispecific molecules we also evaluated one other potential permissive site diametrically opposite the natural CDR-like loops, which was found to be tolerant of peptide insertion. Our data suggest that CTLA-4 is a suitable human scaffold for engineering single-domain molecules with one or possibly more binding specificities. (C) 2000 Federation of European Biochemical Societies.

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=> (CD80 or B7-1) and phage
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L11 7 FILE BIOTECHNO
L12 0 FILE COMPENDEX
L13 0 FILE ANABSTR
L14 0 FILE CERAB
L15 0 FILE METADEX
L16 2055 FILE USPATFULL

TOTAL FOR ALL FILES
L17 2098 (CD80 OR B7-1) AND PHAGE

=> l17 and scFv
L18 3 FILE CAPLUS
L19 1 FILE BIOTECHNO
L20 0 FILE COMPENDEX
L21 0 FILE ANABSTR
L22 0 FILE CERAB
L23 0 FILE METADEX
L24 757 FILE USPATFULL

TOTAL FOR ALL FILES
L25 761 L17 AND SCFV

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L20 HAS NO ANSWERS
L21 HAS NO ANSWERS
L22 HAS NO ANSWERS
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PROCESSING COMPLETED FOR L20
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L26 3 DUP REM L18-L22 (1 DUPLICATE REMOVED)

=> d l26 ibib abs total

L26 ANSWER 1 OF 3 CAPLUS COPYRIGHT 2006 ACS on STN DUPLICATE 1
ACCESSION NUMBER: 2000:240607 CAPLUS
DOCUMENT NUMBER: 133:221373
TITLE: Molecular characterization and applications of recombinant **scFv** antibodies to CD152 co-stimulatory molecule
AUTHOR(S): Pistillo, M. P.; Tazzari, P. L.; Ellis, J. H.; Ferrara, G. B.
CORPORATE SOURCE: Immunogenetics Laboratory, National Cancer Institute Advanced Biotechnology Center, Genoa, 16132, Italy
SOURCE: Tissue Antigens (2000), 55(3), 229-238
CODEN: TSANA2; ISSN: 0001-2815
PUBLISHER: Munksgaard International Publishers Ltd.
DOCUMENT TYPE: Journal
LANGUAGE: English
AB Recombinant human monoclonal antibodies against CD152 have been generated by selecting a synthetic **phage scFv** library with purified CD152-Ig fusion protein. Sixteen **scFv** fragments were isolated which specifically react with CD152 by enzyme-linked immunoabsorbent assay (ELISA) and Western blot resulting in their clustering into two groups recognizing different antigenic determinants.

One group of **scFvs** (#3, #13, #40, #44, #47, #51, #57, #80, #83) recognized an epitope on CD152 dimer whereas another group (#15, #18, #31, #35, #54, #72, #81) recognized an epitope on both dimeric and monomeric CD152 mol. suggesting their possible use in understanding the subunit structure of CD152 which is still controversial. Sequencing of the VH genes revealed that all the **scFvs** belonged to the VH3 gene family but they were different in CDR3 length and composition It was possible to correlate specific CDR3 sequences with reactivity of the two groups of **scFvs**. Four **scFvs**, #3, #40, #81 and #83, each representative of one specific CDR3, were selected for further anal. Competition ELISA expts. showed that they recognize CD152 in its native configuration and bound to different epitopes from the **CD80**/CD86 interaction site. The **scFvs** were able to stain human T lymphocytes stimulated either with anti-CD3 and CD28 antibodies or PHA, PMA and ionomycin by cytofluorimetry suggesting that they can be useful reagents for monitoring the kinetics of surface-bound and intracellular CD152.

REFERENCE COUNT: 27 THERE ARE 27 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L26 ANSWER 2 OF 3 CAPLUS COPYRIGHT 2006 ACS on STN

ACCESSION NUMBER: 1999:673014 CAPLUS
DOCUMENT NUMBER: 131:298647
TITLE: Production of human antibodies to targeted epitopes
INVENTOR(S): Davis, Claude Geoffrey; Jakobovits, Aya
PATENT ASSIGNEE(S): Abgenix, Inc., USA
SOURCE: PCT Int. Appl., 72 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.		DATE
WO 9953049	A1	19991021	WO 1999-US8276		19990414
W: AE, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ, DE, DK, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, UA, UG, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM					
RW: GH, GM, KE, LS, MW, SD, SL, SZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG					
US 2002029391	A1	20020307	US 1998-60743		19980415
AU 9934945	A1	19991101	AU 1999-34945		19990414
EP 1070126	A1	20010124	EP 1999-916685		19990414
R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, FI					
US 2003092125	A1	20030515	US 2002-281387		20021023
PRIORITY APPLN. INFO.:			US 1998-60743	A	19980415
			WO 1999-US8276	W	19990414

AB The authors disclose a method of biasing the immune response of a mammal toward a desired epitope of a chosen antigen, particularly a functionally-relevant epitope. The epitope-biasing method employs iterative screening protocols for **phage** displayed antibodies, functional assays of target antigen, and re-immunization with mimotopes from random peptide libraries. In one example, mice transgenic for human heavy and light chain antibody genes, were immunized with lymphocytes. IgG transcripts from splenocytes were cloned as **scFv** fragments into filamentous **phage** and the recombinants screened for binding to cell-bound L-selectin and inhibition of selectin-mediated adhesion of lymphocytes to vascular endothelium. **Phage**-derived antibodies exhibiting high affinity for cell-bound L-selectin and inhibitory function were screened against a peptide library and the reactive peptides used to immunize transgenic mice for a narrowed immune response.

REFERENCE COUNT: 8 THERE ARE 8 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L26 ANSWER 3 OF 3 CAPLUS COPYRIGHT 2006 ACS on STN
ACCESSION NUMBER: 1999:350741 CAPLUS
DOCUMENT NUMBER: 131:1429
TITLE: Method of identifying epitope-binding binding site domains, multivalent proteins containing them, and their use in diagnosis and as pharmaceuticals
INVENTOR(S): Kufer, Peter; Raum, Tobias; Borschert, Katrin; Zettl, Florian; Lutterbuse, Ralf
PATENT ASSIGNEE(S): Germany
SOURCE: PCT Int. Appl., 152 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 9925818	A1	19990527	WO 1998-EP7313	19981116
W: AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ, DE, DK, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, UA, UG, US, UZ, VN, YU, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM				
RW: GH, GM, KE, LS, MW, SD, SZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG				
CA 2309679	AA	19990527	CA 1998-2309679	19981116
AU 9918731	A1	19990607	AU 1999-18731	19981116
EP 1032660	A1	20000906	EP 1998-963460	19981116
R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, SI, LT, LV, FI, RO				
JP 2002508924	T2	20020326	JP 2000-521184	19981116

PRIORITY APPLN. INFO.: EP 1997-120096 A 19971117
WO 1998-EP7313 W 19981116

AB The present invention relates to a method of identifying binding site domains that retain the capacity of binding to an epitope when positioned C-terminal of at least one further domain in a recombinant bi- or multivalent polypeptide. The present invention further relates to a kit comprising components such as panels of recombinant vectors of bacterial libraries transfected with a panel of recombinant vectors which is useful in carrying out the method of the invention. Furthermore, binding site domains and fusion proteins obtainable by the method of the invention as well as antibody-like mols. comprising such domains and proteins are described. Furthermore, pharmaceutical and diagnostic compns. containing the above-described fusion proteins and polypeptides are provided. Thus, in a **phage** λ-E. coli display system, the N-terminus of the VH domain of **scFv**'s was fused to the N2 domain of the gene III protein while the C-terminus of the VL domain was fused to the CT domain of the gene III protein. In this way, 17-1A-binding **scFv**'s were produced. DNA encoding these **scFv**'s were inserted into a vector containing a fragment of the **CD80** cDNA to prepare expression vectors encoding fusion proteins containing an N-terminal **CD80** extracellular domain fused to the 17-1A antigen-binding **scFv**'s. CHO cells transfected with these vectors produced 17-1A-binding fusion proteins.

REFERENCE COUNT: 8 THERE ARE 8 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT